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WATER QUALITY:

Is *E. coli* Distinct Enough to Join the Hunt?

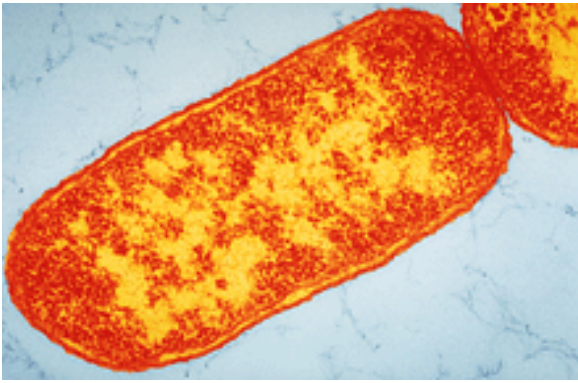
David Malakoff

Underlying many bacterial source-tracking techniques is the assumption that some strains of bacteria are found only within a single kind or group of animals. But the idea of host specificity may be wrong when it comes to the common fecal bacteria *Escherichia coli*, argues David Gordon, a microbiologist at the Australian National University in Canberra. *E. coli* populations are so mercurial, he says, that scientists should think twice before using them for source tracking. But others say that new techniques may still make the bacterium a tracking star.

E. coli is popular with public health scientists because it is common, is easy to culture, and can be deadly in some variants. Until recently, however, few researchers had studied how populations of the bacterium varied by geography and host.

The answer, Gordon says in a May 2001 *Microbiology* review, is that host and place count for little in explaining *E. coli*'s genetic variation. Geographic separation, for instance, could explain just 10% of the differences found in bacteria hosted by rodents in Mexico and Australia; the rest, he says, are due to diet and other factors. Similarly, Australian mammals shared many strains. "There is some host specificity," he says, "but the patterns aren't strong enough to unambiguously assign a strain to a source." Other microbes, says Gordon, may produce better results.

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Fuzzy trail. *E. coli* may not be a good bacterium for source trackers.

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Scientists familiar with bacterial source tracking say that Gordon's caution is justified. But powerful genetic fingerprinting techniques may overcome such problems, says Mansour Samadpour, a University of Washington, Seattle, public health specialist who has pioneered molecular source-tracking methods using *E. coli*. "Sensitive methods can identify differences in bacteria that may otherwise appear identical," he notes.

Valerie Jody Harwood, of the University of South Florida in Tampa, urges source trackers to adopt "a strong population biology perspective." It may be impractical to prove that a specific bacterium came from a specific source, she says. "But we probably can show that one set of strains is more likely to come from one host than another"--or at least determine if they came from a human source. That ability, she says, would be enough to keep *E. coli* in the source trackers' toolbox.

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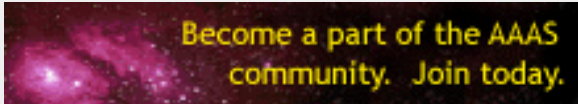
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